

# SEQUENCE LISTING

<110> Lechler, Robert I.  
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION SIGNAL 2 (B7/CD28 INTERACTION)

<130> 2292/0H795

<140> US 09/674,462

<141> 2001-05-08

<150> PCT/ GB99/01350

<151> 1999-04-30

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 223

<212> PRT

<213> Sus scrofa

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Val	Phe	Ser	Lys	Gly	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	35	40	45	
Asn	Ser	Arg	Gly	Val	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Gly	Ser	Ala	Gly	50	55	60	
Lys	Ala	Ala	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Arg	Ala	Gly	Ser	Gln	65	70	75	80
Met	Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Thr	Val	Glu	Asp	Glu	Leu	Thr	85	90	95	
Phe	Leu	Asp	Asp	Ser	Thr	Cys	Thr	Gly	Thr	Ser	Thr	Glu	Asn	Lys	Val	100	105	110	
Asn	Leu	Thr	Ile	Gln	Gly	Leu	Arg	Ala	Val	Asp	Thr	Gly	Leu	Tyr	Ile	115	120	125	

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly  
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Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
 165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
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Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
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<212> DNA

<213> Sus scrofa

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<212> PRT

<213> Artificial Sequence

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<223> pCTLA4-Ig construct (Figure 4)

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 Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala  
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 Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly  
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 Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln  
 65 70 75 80  
 Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr  
 85 90 95  
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 Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly  
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 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
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 Asp Gly Gly Ser Gly Gly Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr  
 165 170 175  
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
 180 185 190  
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg  
 195 200 205  
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
 210 215 220  
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
 225 230 235 240  
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
 245 250 255  
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 260 265 270  
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
 275 280 285

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 ctccaggga ggggctggag tgggtctcag ctattcgtgg tagtggtggg agcacatact 180  
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 <212> PRT  
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35 40 45

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50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Ala Gly Arg Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
115 120 125

Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly  
130 135 140

Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn  
145 150 155 160

Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
165 170 175

Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro  
180 185 190

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile  
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<211> 729  
<212> DNA  
<213> Phage library

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<210> 9

<211> 729

<212> DNA

<213> Phage library

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atctgggaca gaattcactc tcacaatcag cagcctgcag cctgaagatt ttgcaactta 660
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<210> 10

<211> 240

<212> PRT

<213> Phage library

<400> 10

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Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50              55              60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

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Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
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Thr	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	Asn
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Pro	Lys	Leu	Leu	Ile	Tyr	Arg	Asn	Asn	Gln	Arg	Pro	Ser	Gly	Val	Pro
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Ser	Gly	Leu	Arg	Ser	Glu	Asp	Glu	Ala	Ser	Tyr	Tyr	Cys	Ala	Ala	Trp
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 35 40 45



Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn  
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 65 70 75 80  
 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95  
 Tyr Tyr Cys Ala Arg Met Arg Lys Asp Lys Phe Asp Tyr Trp Gly Gln  
 100 105 110  
 Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
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 Gly Ser Gly Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser  
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 Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser  
 145 150 155 160  
 Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro  
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 Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser  
 180 185 190  
 Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser  
 195 200 205  
 Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Val  
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 Thr Val Leu Gly Ala Ala  
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 Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe  
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 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr  
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 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Val Ala Pro Tyr Val Asn Thr Leu Val Phe Trp Gly Gln Gly  
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 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
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 130 135 140  
 Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser  
 145 150 155 160  
 Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
 165 170 175  
 Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro  
 180 185 190  
 Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile  
 195 200 205  
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 Leu Gly

<210> 13  
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<400> 13

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Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
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Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Leu	Asn	
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<210> 15  
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<400> 15  
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 50 55 60  
 Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln  
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 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile  
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Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly  
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
165 170 175

Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
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Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
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Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
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